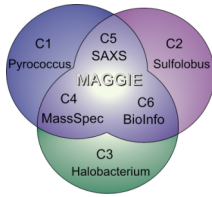


Computational Analysis of the Protein Interaction Networks of Three Archaeal Microbes



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The computational identification and mapping of protein complexes and networks using genomic and experimental data is critical to our understanding of complex biological systems. In relation to the MAGGIE project to characterize the molecular machines and interactions of archaeal genomes, we have developed a software suite for analysis of their protein interaction network. These algorithms identify missing links in the network by transitive closure, extracted protein complexes as cliques, placed them into context by a hierarchical decomposition process using a distance metric and allowed for proteins to be shared between complexes. Finally, we have developed an algorithm for extracting bicliques from a data matrix and applied it to finding bicliques between protein domains and protein complexes.

Because of the abundance of experimental data, we have used yeast in development and testing of these programs, but as experiments proceed on microbial proteomes, we have begun to apply these approaches to *Pyrococcus furiosus*, *Sulfolobus solfataricus*, and *Halobacterium* NRC-1. An advantage to studying these three diverse archaea is the capability to characterize conserved components and organism specific systems of the microbial domain. This software and results drawn from analysis of these organisms will be made available to the GTL community.